

SEQUENCE LISTING

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Vogel, Monique
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<120> POLYPEPTIDES CAPABLE OF FORMING ANTI~~GEN~~^{IN} ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE

<130> 6816/P63221US0

<140> 09/147,443
<141> 1999-01-21

<150> PCT/EP97/03253
<151> 1997-06-20

<150> EP 96810421.6
<151> 1996-06-24

<160> 64

<170> PatentIn Ver. 2.1

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tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat  96
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
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 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
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   65          70          75          80

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ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat tgt 288
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 85 90 95

gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac atg 336
 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Met
 100 105 110

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 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro
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gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn	
20 25 30	
tgg tat cag cag aaa cca ggg aaa gcc cct aag ttg ctg atc tat ggt	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly	
35 40 45	
gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat	240
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
65 70 75 80	
ttt gca act tac tac tgt caa gag agt tac agt aat cct cta atc acc	288
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr	
85 90 95	
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Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
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Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1	5				10					15						

tcc	ctg	aga	ctc	tcc	tgt	gaa	gcg	tct	gga	ttc	gcc	ctc	aga	agt	tct	96
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Ala	Leu	Arg	Ser	Ser	
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ggc	atg	cac	tgg	gtc	cgc	cag	gct	cct	ggc	aag	ggg	ctg	gag	tgg	gtg	144
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gca	ctt	ata	tgg	ttt	gat	gga	agt	atc	aga	tcg	tat	gca	gaa	tcc	gtg	192
Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
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aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	act	tcc	aag	aac	acc	cta	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
65				70					75						80	

ctc	caa	atg	cgc	agt	ctg	agt	gcc	gac	acg	gct	gtg	tat	tac	tgt	288	
Leu	Gln	Met	Arg	Ser	Leu	Ser	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85					90					95						

gcg	aga	gac	aag	gog	gtt	cgg	gga	att	agc	agg	tac	aac	tat	tac	atg	336
Ala	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
100					105					110						

gac	gtc	tgg	ggc	aaa	ggg	acc	acg	gtc	acc	gtc	tcc	tca			375	
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20					25					30						

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35					40					45						

Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
50					55					60						

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<210> 7

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gtc acc atc act tgc cgg gca agt cag aac att atc cgc tat tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn	
20 25 30	

tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	
35 40 45	

gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	

tct ggg aca gat ttc act ctc acc atc agt agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr	
85 90 95	

ttc ggc cct ggg acc aaa gtg gag atc aaa	318
Phe Gly Pro Gly Thr Lys Val Glu Ile Lys	
100 105	

<210> 8

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<213> Homo sapiens

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 35 40 45
 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
 85 90 95
 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
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 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gct aga gac aag gct gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

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 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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gtc acc atc acc tgc cgg gca agt cag agt atc atc agg tat ttg aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

tgg tat cag cac aaa cca gga aaa gcc cct aaa ctc ctc atc ttt gct 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala
35 40 45

gca tcg aat ttg caa act ggg gtc cca tcc agg ttc agt ggc agt gga 192
Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

tct ggg aca gat ttc act ctc acc atc agt gac ctg cag cct gag gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
65 70 75 80

ttc gca act tac tac tgt caa cag agt tac agt agg ccg ttc act ttt 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

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Gly Arg Gly Thr Ser Leu Asp Ile Lys
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20 25 30

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35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

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Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1	5						10					15				

tcc	ctg	aga	ctc	tcc	tgt	ata	gcg	tct	gga	ttc	acc	ctc	agg	aat	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Asn	Tyr	
20						25						30				

gcc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35						40					45					

gca	ggt	ata	tgg	ttt	gat	gga	agc	aac	aaa	aac	tat	gca	gac	tcc	gtg	192
Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Asn	Tyr	Ala	Asp	Ser	Val	
50					55					60						

aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aac	tcc	aag	aac	act	ctg	ttt	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
65					70					75			80			

ctg	cac	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	aca	tat	tac	tgt	288
Leu	His	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	
85					90					95						

gcg	aga	gag	agg	gcg	att	cgg	gga	atc	agt	aga	tac	aat	tac	tac	atg	336
Ala	Arg	Glu	Arg	Ala	Ile	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
100					105					110						

gac	gtc	tgg	ggc	aag	ggg	acc	acc	acg	gtc	acc	gtc	tcc	tca		375
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115					120					125					

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<213> Homo sapiens

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20						25					30					

Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35					40					45						

Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Asn	Tyr	Ala	Asp	Ser	Val	
50					55					60						

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
65					70					75			80			

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

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1 5 10 15	

gtc acc atc act tgc cgg gca agt cag agc att cga agc tct tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn	
20 25 30	

tgg tat cag cag aaa cca ggg aaa gcc cct aaa gtc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala	
35 40 45	

gca tcc agt ttg caa agt ggg gtc cca tcc agg ttc agt ggc aga gga	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly	
50 55 60	

tct ggg aca gat ttc act ctc acc atc agc agt ctg caig cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gcg act tat tat tgt caa cag agt tcc agt tcc tcg tgg acg ttc	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe	
85 90 95	

ggc caa ggg acc aag gtg gaa atc aaa	315
Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

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<213> Homo sapiens

<400> 16

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 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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Gln	Val	Lys	Leu	Leu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys			
1	5								10					15			

tcc ctg aga ctt tcc tgt gca gcg tct gga ttc agt ttc aat agc cat
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His
 20 25 30

ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg		144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
35	40													45			

gca ttt ata tgg ttt gat ggc agt aat aaa tac tat gca gac tcc gtg
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag	ggc	cga	tcc	acc	atc	acc	aga	gac	aac	tcc	aag	aac	acg	ctg	tat		240
Lys	Gly	Arg	Phe	Thr	Ile	Thr	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
65	70													80			

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg	aga	gag	acc	tca	gta	agg	cta	ggg	tat	agc	cgc	tac	aat	tac	tac		336
Ala	Arg	Glu	Thr	Ser	Val	Arg	Leu	Gly	Tyr	Ser	Arg	Tyr	Asn	Tyr	Tyr		
100									105				110				

<210> 18
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Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys
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20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Tyr Asn Tyr Tyr
100 105 110

<210> 19
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<220>
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<222> (1) .. (318)

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gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
   1           5           10          15

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 20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45

gca tcc agt ttg caa ggt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tat tac tgt caa cag agt tac agg gcc cct cag tgg acg 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95

ttc ggc caa ggg acc aag gtg gaa atc aaa 318
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 20
<211> 106
<212> PRT
<213> Homo sapiens

<400> 20
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 21
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

<400> 21

cag	gtg	aaa	ctg	ctc	gag	tct	ggg	gga	ggc	gtg	gtc	cag	ccg	ggg	ggg		48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
1			5						10			15					
tcc	ctg	aga	ctc	tcc	tgt	gta	gcg	tct	gga	ttc	acc	ctc	agg	agt	tat		96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr		
20									25					30			
ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggc	ctg	gag	tgg	gtg		144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
35								40				45					
gct	ttt	ata	tgg	ttt	gat	gga	agt	aat	aaa	gga	tat	gta	gac	tcc	gtg		192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val		
50								55			60						
aag	ggc	cga	ttc	acc	atc	tcc	cga	gac	aat	tcc	aag	aac	atg	gtc	tat		240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr		
65								70			75			80			
ctg	caa	atg	aac	agc	ctg	aga	gcc	gat	gac	acg	gct	gta	tat	tat	tgt		288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
85								90					95				
gcg	aga	gag	aag	gcg	ctt	cgg	gga	atc	agc	aga	tac	aac	tat	tac	ctg		336
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu		
100								105				110					
gac	gtc	tgg	ggc	aag	ggg	acc	acc	acg	gtc	acc	gtc	tcc	tca			375	
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Thr	Val	Ser	Ser			
115								120				125					

<210> 22

<211> 125

<212> PRT

<213> Homo sapiens

<400> 22

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly			
1			5						10			15					
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr		
20									25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
35								40				45					
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val		
50								55			60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr		
65								70			75			80			
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
85								90			95						

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 23
 <211> 333
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(333)

<400> 23
 gtg gtg act cag cca ccc tca gcg tct ggg acc ccc gga cag agg gtc 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1 5 10 15

acc atc tct tgt tct gga agc aac tcc atc ctt gga agt aag tat gta 96
 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val
 20 25 30

tac tgg tac cag aaa ctc cca gga acg gcc ccc aaa ctc ctc atc tat 144
 Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45

aag aat gat cag cgg ccc tca ggg gtc tct gac cga ttc tct ggc tcc 192
 Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser
 50 55 60

aag tct ggc acc tcg gcc tcc ctg gcc atc agt ggg ctc cgg tcc gag 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu
 65 70 75 80

gat gag gct gac tat tac tgt gca cca tgg gat gcc aac ctg ggt ggc 288
 Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly
 85 90 95

ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc 333
 Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 100 105 110

<210> 24
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 24
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val
 20 25 30

Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45

Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser
 50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly
 85 90 95

Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 100 105 110

<210> 25

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(375)

<400> 25

cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gaa gca tct gga ttc acc ctc aga agt tct 96
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 26
<211> 125
<212> PRT
<213> Homo sapiens

<400> 26
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 27
<211> 312
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(312)

<400> 27
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cgg aca agt cag acc att agc aga aat tta aat 96
Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn
20 25 30
tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45
aca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

tct ggg aca gat ttc act ctc acc atc aat agt cta caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc cct tcg ttc ggc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly
 85 90 95

caa ggg acc aag gtg gaa atc aaa 312
 Gln Gly Thr Lys Val Glu Ile Lys
 100

<210> 28
<211> 104
<212> PRT
<213> Homo sapiens

<400> 28
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly
 85 90 95

Gln Gly Thr Lys Val Glu Ile Lys
 100

<210> 29
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (375)

<400> 29
cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat	96		
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr			
20	25	30	
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg	144		
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg	192		
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val			
50	55	60	
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg ctc tat	240		
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr			
65	70	75	80
ctg caa atg aat agc ctg aga gcc gag gac acg gct gta tat tat tgt	288		
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg	336		
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu			
100	105	110	
gac gtc tgg ggc aag ggg gcc acg gtc acc gtc tcc tca	375		
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser			
115	120	125	

<210> 30

<211> 125

<212> PRT

<213> Homo sapiens

<400> 30

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr		
20	25	30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val		
50	55	60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr			
65	70	75	80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu		
100	105	110

Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser		
115	120	125

<210> 31
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(318)

<400> 31 48
gtg atg acc cag tct cca tcc tcc ctg tct gca tct ata ggc gac aga Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
gtc acc atc act tgc cgg gca agt cag agc gtt acc agg tct tta aat 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
20 25 30
tgg tat cag cag aaa cca ggg aaa gcc cct agg ctc cta atc ttt gct 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
35 40 45
gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
tct ggg aca gat ttc acc ctc acc atc agc agt ctg caa cct gag gat 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
ttt gga act tac tac tgt caa cag aat tac agg acc cct cag tgg acg 288
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
85 90 95
ttc ggc caa ggg acc aag gta gaa atc aaa 318
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 32
<211> 106
<212> PRT
<213> Homo sapiens

<400> 32
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
35 40 45
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 33
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

<400> 33
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tat 288
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
 85 90 95

tgt gcg aga gag aag gcg ctt cgg gga atc agc aga tac aac tat tac 336
 Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
 100 105 110

ctg gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 378
 Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 34
 <211> 126
 <212> PRT

<213> Homo sapiens

<400> 34

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly
1															
														10	15

Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr	
														20	25	30

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
														35	40	45

Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
														50	55	60

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr		
														65	70	75	80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Tyr	
														85	90	95

Cys	Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	
														100	105	110

Leu	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser			
														115	120	125

<210> 35

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(333)

<400> 35

gtg	gtg	act	cag	gag	ccc	tca	ctg	act	gtg	tcc	cca	gga	ggg	aca	gtc	
Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Thr	Val	Ser	Pro	Gly	Gly	Thr	Val	
1															15	

act	ctc	acc	tgt	gct	tcc	agc	act	ggg	gca	gtc	acc	agg	ggt	tac	tat		
Thr	Leu	Thr	Cys	Ala	Ser	Ser	Thr	Gly	Ala	Val	Thr	Arg	Gly	Tyr	Tyr		
															20	25	30

cca	aac	tgg	ttc	cag	cag	aag	cct	gga	caa	gca	ccc	agg	gca	ctg	att		
Pro	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Ala	Leu	Ile		
															35	40	45

tat	agt	aca	aac	aaa	aaa	cac	tcc	tgg	acc	cct	gcc	cgg	ttc	tca	ggc		
Tyr	Ser	Thr	Asn	Lys	Lys	His	Ser	Trp	Thr	Pro	Ala	Arg	Phe	Ser	Gly		
															50	55	60

tcc	ctc	ctt	ggg	ggc	aaa	gct	gcc	ctg	aca	ctg	tca	ggc	gtt	cag	cct			
Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu	Thr	Leu	Ser	Gly	Val	Gln	Pro			
															65	70	75	80

gaa gac gag gct gaa tat tac tgc ctg ctc tac tat ggt ggt gct caa	288
Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln	
85	90
	95

ctc gta ttc ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc	333
Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro	
100	105
	110

<210> 36
<211> 111
<212> PRT
<213> Homo sapiens

<400> 36	
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val	
1	5
	10
	15

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr	
20	25
	30

Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile	
35	40
	45

Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly	
50	55
	60

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro	
65	70
	75
	80

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln	
85	90
	95

Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro	
100	105
	110

<210> 37
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (375)

<400> 37	
cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1	5
	10
	15

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	
20	25
	30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg qag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 38

<211> 125

<212> PRT

<213> Homo sapiens

<400> 38

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 39
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(315)

<400> 39

gtg ttg acc cag tct cca tcc tcc ctg tct gca tct ata cga gac aga	48
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg	
1 5 10 15	

gtc acc atc act tgc cgg gca agt cag aac att ggc agt tat tta aat 96

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn	
20 25 30	

tgg tat cag cac aaa cca ggg aca gcc cct aaa ctc ctg atc tat gct 144

Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	

gta tcc gct ttg caa agt ggg gtc cca tcg agg ttc agt ggc agt aga 192

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg	
50 55 60	

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gca act tac tac tgt caa cag agt tac agt ccc ccg tac act ttc 288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe	
85 90 95	

ggc cag ggg acc aac ctg cag atc aaa 315

Gly Gln Gly Thr Asn Leu Gln Ile Lys	
100 105	

<210> 40
<211> 105
<212> PRT
<213> Homo sapiens

<400> 40

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg	
1 5 10 15	

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn

20 25 30	
----------	--

Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45	
----------	--

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg

50 55 60	
----------	--

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys
 100 105

<210> 41
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (375)

<400> 41
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 42
<211> 125
<212> PRT
<213> Homo sapiens

<400> 42

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly
1				5					10			15		

Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe
			20					25				30			

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35				40							45			

Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val
	50				55				60						

Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
	65				70				75				80		

Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85			90						95			

Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met
				100			105					110			

Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser			
		115				120					125				

<210> 43

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(315)

<400> 43

gtg	atg	acc	cag	tct	cca	tcc	tcc	ctg	tct	gca	tct	gtg	gga	gac	aga	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10				15			

gtc	acc	atc	act	tgc	cgg	gca	agt	cag	agc	att	atc	aac	aat	tta	aat	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Asn	Asn	Leu	Asn	
			20					25				30				

tgg	tat	cag	cag	aaa	cca	ggc	aaa	gcc	cct	gaa	ctc	ctg	atc	tat	gct	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Glu	Leu	Leu	Ile	Tyr	Ala	
			35			40						45				

gca	tcc	agt	ttg	caa	agt	ggg	gtc	cct	tca	agg	ttc	cgt	ggc	agt	gga	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Arg	Gly	Ser	Gly	
			50			55				60						

tct	ggg	aga	gat	ttc	act	ctc	acc	gtc	acc	agt	ctg	caa	cct	gaa	gat	240
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Val	Thr	Ser	Leu	Gln	Pro	Glu	Asp	
			65			70				75			80			

ttt gca act tac tac tgt caa cag agt tac agt acc ctg tgg acg ttc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
 85 90 95

ggc caa ggg acc aag gtg gaa atc aaa 315
 Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 44
<211> 105
<212> PRT
<213> Homo sapiens

<400> 44
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
 50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 45
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

<400> 45
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60	192
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80	240
ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110	336
gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	375
<210> 46	
<211> 125	
<212> PRT	
<213> Homo sapiens	
<400> 46	
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 20 25 30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80	
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110	
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	
<210> 47	
<211> 315	
<212> DNA	
<213> Homo sapiens	

<220>
<221> CDS
<222> (1)..(315)

<400> 47
 gtg atg acc cag tct cca ttc tcc ctg tct gca tct gta gga gac aga 48
 Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

 gtc acc atc act tgc cg^g gca agt cag aac att agg agt ttt tta agt 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
 20 25 30

 tgg tat cag cag aaa cca ggg aca gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

 gca tcc agg ttg caa agt ggg gtc cca tca agg ttc agt ggc agt ggg 192
 Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

 tct ggg aca gat ttc act ctc acc atc agc act ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp
 65 70 75 80

 ttt gcg act tac tac tgt caa cag agt tac agt gcc cct tgg acg ttc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe
 85 90 95

 ggc caa ggg acc aag ctg gaa atc aaa 315
 Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 48
<211> 105
<212> PRT
<213> *Homo sapiens*

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<400> 48
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
      1          5          10          15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
      20         25          30

Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala
      35         40          45

Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
      50         55          60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp
      65         70          75          80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe
      85         90          95

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Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 49
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (375)

<400> 49
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc tcc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110
 gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 50
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 50
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 51

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(315)

<400> 51

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc cga ttc act ttc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
 85 90 95

ggc cct ggg acc aaa gtg gat atc aaa Gly Pro Gly Thr Lys Val Asp Ile Lys 100 105	315
<210> 52	
<211> 105	
<212> PRT	
<213> Homo sapiens	
<400> 52	
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45	
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 85 90 95	
Gly Pro Gly Thr Lys Val Asp Ile Lys 100 105	
<210> 53	
<211> 384	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (1)...(384)	
<400> 53	
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15	48
tcc ctg aga ctt tcc tgt gca gcg tct gga ttt acc ttc agt agc tat Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30	96
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
gca gat ata tgg ttt gat gga ggt aat aaa cat tat gca gac ttc gtg Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 55 60	192

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg gtg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

cta caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg agg gat tac tat agc gtt act aag aaa ctc aga ctc cac tac tac 336
 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110

tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 384
 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 54
<211> 128
<212> PRT
<213> Homo sapiens

<400> 54
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 55
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(315)

<400> 55

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1	5
	10
	15

gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat tta acc	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr	
20	25
	30

tgg tat cag caa aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr Ala	
35	40
	45

gca tcc aat tta caa agt ggg gtc cca tca agg ttc agc ggc agt gga	192
Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60

tct ggc aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65	70
	75
	80

ttt gca act tat tac tgt cta caa gat aac aat ttc ccg tac act ttt	288
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe	
85	90
	95

ggc cag ggg acc aag ctg gag atc aaa	315
Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100	105

<210> 56

<211> 105

<212> PRT

<213> Homo sapiens

<400> 56

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1	5
	10
	15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr	
20	25
	30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr Ala	
35	40
	45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65	70
	75
	80

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe	
85	90
	95

Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100	105

<210> 57
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)

<400> 57

cag	gtg	aaa	ctg	ctc	gag	tct	ggg	gga	ggc	gtg	gtc	cag	ccg	ggg	ggg		48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
1	5						10					15					

tcc

ctg	aga	gtc	gcc	tgt	gta	gcf	tct	gga	ttc	acc	ttc	agg	aat	ttt		96	
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe		
20							25					30					

ggc

atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg		144	
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
35							40					45					

gct

ttt	att	tgg	ttt	gat	gca	agt	aat	aaa	gga	tat	gga	gac	tcc	gtt		192	
Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val		
50							55					60					

aag

ggc	cga	ttc	acc	gtc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctc	tat		240	
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
65							70					75			80		

ctg

caa	atg	aac	ggc	ctg	aga	gcc	gaa	gac	acg	gct	gta	tat	tat	tgt		288	
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
85							90					95					

gcg

aga	gag	aag	gog	gtt	cgg	gga	att	agt	aga	tac	aac	tac	tac	atg		336	
Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met		
100							105					110					

gac

gtc	tgg	ggc	aag	ggg	acc	acg	gtc	acc	gtc	tcc	tca				375	
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
115							120					125				

<210> 58
<211> 125
<212> PRT
<213> Homo sapiens

<400> 58

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
1			5						10			15				

Ser

Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe		
20							25					30				

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 59
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(315)

<400> 59

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	

gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn	
20 25 30	

tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat act	144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr	
35 40 45	

gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val	
50 55 60	

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe	
85 90 95	

ggc cag ggg acc aag ctg cag atc aaa	315
Gly Gln Gly Thr Lys Leu Gln Ile Lys	
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 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

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 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn	
20 25 30	

tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat gct	144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala	
35 40 45	

gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val	
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tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe	
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ggc cag ggg acc aag ctg cag atc aaa	315
Gly Gln Gly Thr Lys Leu Gln Ile Lys	
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20 25 30	

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala	
35 40 45	

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val	
50 55 60	

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe	
85 90 95	

Gly Gln Gly Thr Lys Leu Gln Ile Lys	
100 105	